Amendments to the Claims:

All amendments and cancellations are made without prejudice or disclaimer. This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1. (Original) A B Lymphocyte Stimulator (BLyS) binding polypeptide comprising the amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.

2. (Original) The polypeptide according to claim 1, wherein Xaa is Pro or Ser.

3. (Currently amended) The polypeptide according to claim 1, wherein said polypeptides comprises the amino acid sequence: X_1-X_2-Asp-X_4-Leu-Thr-X_7-Leu-X_9-X_{10} (SEQ ID NO:448),

wherein

X_1 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X_2 is Tyr, Phe, Glu, Cys, **or** Asn;

X_4 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X_7 is Lys, Asn, Gln, Gly, or Arg;

X_9 is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and

X_{10} is Leu, Phe, Val, Ile, or His.

4. (Original) The polypeptide according to claim 3, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

5. (Currently amended) The polypeptide according to claim 3, wherein said polypeptide comprises the amino acid sequence: Ala-X_2-X_3-X_4-Asp-X_6-Leu-Thr-X_9-Leu-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO:447),

wherein

X_2 is any amino acid except Arg;

X_3 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X_4 is Tyr, Phe, Glu, Cys, **or** Asn;

X_6 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X_9 is Lys, Asn, Gln, Gly, or Arg;

X_{11} is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X_{12} is Leu, Phe, Val, Ile, or His;

X_{13} is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X_{14} is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

6. (Original) The polypeptide according to claim 3, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:186-435 as depicted in Table 14.

7. (Original) The polypeptide according to claim 3, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:437-444 as depicted in Table 15.

8. (Currently amended) The polypeptide according to claim 1, comprising an amino acid sequence selected from the group consisting of:

~~Ala-Gly-Lys-Glu-Pro-Cys-Tyr-Phe-Tyr-Trp-Glu-Cys-Ala-Val-Ser-Gly (SEQ ID NO:450);~~

Ala-Gly-Val-Pro-Phe-Cys-Asp-Leu-Leu-Thr-Lys-His-Cys-Phe-Glu-Ala-Gly (SEQ ID NO:451);

Gly-Ser-Ser-Arg-Leu-Cys-His-Met-Asp-Glu-Leu-Thr-His-Val-Cys-Val-His-Phe-A- la-Pro (SEQ ID NO:452);

Gly-Asp-Gly-Gly-Asn-Cys-Tyr-Thr-A- sp-Ser-Leu-Thr-Lys-Leu-His-Phe-Cys-Met-Gly-Asp-Glu (SEQ ID NO:453);

Gly-Tyr-Asp-Val-Leu-Thr-Lys-Leu-Tyr-Phe-Val-Pro-Gly-Gly (SEQ ID NO:454);

Trp-Thr-Asp-Ser-Leu-Thr-Gly-Leu-Trp-Phe-Pro-Asp-G-ly-Gly (SEQ ID NO:455);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Ly- s-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:186);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:456);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:457);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Val (SEQ ID NO:189);

Ala-Asn-Trp-Phe-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:309);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Ser-Leu-Pro-Asp (SEQ ID NO:458);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Phe-Pro-Asp (SEQ ID NO:353); **and**

Ala-Asn-Trp-Tyr-Asp-Ser-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:327).

9. (Currently amended) A BLyS binding polypeptide comprising an amino acid sequence according to one of the following formulae:

(H) ~~Cys-X_2-Phe-X_4-Trp-Glu-Cys~~ **Cys-X_5-Phe-X_7-Trp-Glu-Cys** (**residues 4-10 of** SEQ ID NO:[[8]]**1**),

wherein

[[X_2]] **X_5** is Phe, Trp, or Tyr; and

[[X_4]] **X_7** is Pro or Tyr; or

(I) Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (SEQ ID NO:9),

wherein

X_2 is Asp, Ile, Leu, or Tyr;

X_3 is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X_4 is His, Leu, Lys, or Phe;

X_5 is Leu, Pro, or Thr;

X_6 is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp; and

X_7 is Ala, Asn, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val; or

(J) Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (SEQ ID NO:10),

wherein

X_2 is Asn, Asp, Pro, Ser, or Thr;

X_3 is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X_4 is Ala, Ile, Leu, Pro, Thr, or Val;

X_5 is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X_6 is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X_7 is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp; **and**

X_8 is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr; or

(K) Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-Cys (SEQ ID NO:11),

wherein

X_2 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X_3 is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X_4 is Asp, His, Leu, or Ser;

X_5 is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X_6 is Ala, Arg, Asn, or Leu;

X_7 is Ile, Leu, Met, Pro, Ser, or Thr;

X_8 is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr; **and**

X_9 is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val; or

(L) Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (SEQ ID NO:12),

wherein

X_2 is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X_3 is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X_4 is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X_5 is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;

X_6 is Asp, Leu, Pro, Thr, or Val;

X_7 is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;

X_8 is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;

X_9 is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;

X_{10} is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr; and

X_{11} is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val.

10. (Currently amended) The polypeptide according to claim 9, wherein

(a) said polypeptide comprises an amino acid sequence of the formula: ~~Cys-X_2-Phe-X_4-Trp-Glu-Cys~~ **Cys-X_5-Phe-X_7-Trp-Glu-Cys** (**residues 4-10 of** SEQ ID NO:[[8]]**1**), and the following amino acid positions are independently selected as follows: X_2 is Tyr; X_4 is Pro; or combinations of such selections; or

(b) said polypeptide comprises an amino acid sequence of the following formula: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (SEQ ID NO:9), and the following amino acid positions are independently

selected as follows: X_2 is Asp or Leu; X_3 is Glu or Leu; X_4 is His or Leu; X_5 is Thr or Pro; X_6 is Lys; or combinations of such selections; or

(c) said polypeptide comprises an amino acid sequence of the following formula: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (SEQ ID NO:10), and the following amino acid positions are independently selected as follows: X_2 is Asp; X_3 is Ile; X_4 is Val or Leu; X_5 is Thr; X_6 is Leu; X_8 is Ser; or combinations of such selections; or

(d) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-Cys (SEQ ID NO:11), and the following amino acid positions are independently selected as follows: X_4 is Asp; X_5 is Glu or Pro; X_6 is Leu; X_7 is Thr; or combinations of such selections; or

(e) said polypeptide comprises an amino acid sequence of the following formula: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (SEQ ID NO:12), and the following amino acid positions are independently selected as follows: X_2 is Trp, Tyr, or Val; X_3 is Asp; X_4 is Asp; X_5 is Leu; X_6 is Leu or Thr; X_7 is Lys or Thr; X_8 is Arg or Leu; X_9 is Thr or Trp; X_{10} is Met or Phe; X_{11} is Val; or combinations of such selections.

11. (Original) A BLyS binding polypeptide comprising an amino acid sequence of the following formula:

(A) X_1-X_2-X_3-Cys-X_5-Phe-X_7-Trp-Glu-Cys-X_{11}-X_{12}-X_{13} (SEQ ID NO:1),

wherein

X_1 is Ala, Asn, Lys, or Ser;

X_2 is Ala, Glu, Met, Ser, or Val;

X_3 is Ala, Asn, Lys, or Pro;

X_5 is Phe, Trp, or Tyr;

X_7 is Pro or Tyr;

X_{11} is Ala, Gln, His, Phe, or Val;

X_{12} is Asn, Gln, Gly, His, Ser, or Val; and

X_{13} is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (SEQ ID NO:2), wherein

X_1 is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X_2 is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X_5 is Asp, Ile, Leu, or Tyr; X_6 is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X_7 is His, Leu, Lys, or Phe; X_8 is Leu, Pro, or Thr;

X_9 is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X_{10} is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X_{12} is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X_{13} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X_{14} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) X_1-X_2-X_3-Cys_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (SEQ ID NO:3),

wherein

X_1 is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X_2 is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X_3 is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X_5 is Asn, Asp, Pro, Ser, or Thr;

X_6 is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X_7 is Ala, Ile, Leu, Pro, Thr, or Val;

X_8 is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X_9 is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X_{10} is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X_{11} is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X_{13} is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X_{14} is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X_{15} is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-Cys-X_{14}-X_{15}-X_{16} (SEQ ID NO:4),

wherein

X_1 is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X_2 is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X_3 is Asn, Asp, Leu, Pro, Ser, or Val;

X_5 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X_6 is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X_7 is Asp, His, Leu, or Ser;

X_8 is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X_9 is Ala, Arg, Asn, or Leu;

X_{10} is Ile, Leu, Met, Pro, Ser, or Thr;

X_{11} is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X_{12} is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X_{14} is Asp, Gly, Leu, Phe, Tyr, or Val;

X_{15} is Asn, His, Leu, Pro, or Tyr; and X_{16} is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:5),

wherein

X_1 is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X_2 is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X_3 is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;

X_5 is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X_6 is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X_8 is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;

X_9 is Asp, Leu, Pro, Thr, or Val;

X_{10} is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;

X_{11} is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;

X_{12} is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;

X_{13} is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;

X_{14} is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;

X_{16} is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;

X_{17} is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F) X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO:6),

wherein

X_1 is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;

X_2 is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;

X_3 is Ala, Asp, Lys, Phe, Thr, Trp or Tyr;

X_4 is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;

X_5 is Asp, Leu, Lys, Phe, Pro, Ser, or Val;

X_6 is His, Ile, Leu, Pro, Ser, or Thr;

X_7 is Arg, Gly, His, Leu, Lys, Met, or Thr;

X_8 is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;

X_9 is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;

X_{10} is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;

X_{11} is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and

X_{12} is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G) X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO:7),

wherein

X_1 is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;

X_2 is Arg, Gln, His, Ile, Leu, or Pro;

X_3 is Asp, Gly, Ile, Lys, Thr, Tyr or Val;

X_4 is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;

X_5 is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;

X_6 is Asp, Glu, His, Leu, Lys, Pro, or Val;

X_7 is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;

X_8 is Gln, Gly, His, Leu, Met, Ser, or Thr;

X_9 is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;

X_{10} is Ala, Gly, Ile, Leu, Lys, Met, or Phe;

X_{11} is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;

X_{12} is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and

X_{13} is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

12. (Original) The BLyS binding polypeptide according to claim 11, wherein

(a) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-Cys-X_5-Phe-X_7-Trp-Glu-Cys-X_{11}-X_{12}-X_{13} (SEQ ID NO:1), and the following amino acid positions are independently selected as follows: X_3 is Lys; X_5 is Tyr; X_7 is Pro; X_{11} is Ala, Gln, His, Phe, or Val; X_{12} is Asn, Gln, Gly, His, Ser, or Val; X_{13} is Ala, Asn, Gly, Ile, Pro, or Ser; or combinations of such selections; or

(b) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (SEQ ID NO:2), and the following amino acid positions are independently selected as follows: X_3 is Asp; X_5 is Asp or Leu; X_6 is Glu or Leu; X_7 is His or Leu; X_8 is Thr or Pro; X_9 is Lys; or combinations of such selections; or

(c) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (SEQ ID NO:3), and the following amino acid positions are independently selected as follows: X_3 is Ala; X_5 is Asp; X_6 is Ile; X_7 is Val or Leu; $X_8$is Thr; X_9 is Leu; X_{11} is Ser; X_{13} is Val; X_{15} is Glu or Pro; or combinations of such selections; or

(d) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-Cys-X_{14}-X_{15}-X_{16} (SEQ ID NO:4), and the following amino acid positions are independently selected as follows: X_1 is Ser; X_2 is Arg; X_3 is Asn or Asp; X_7 is Asp; X_8 is Glu or Pro; X_9 is Leu; X_{10} is Thr; X_{14} is Leu; X_{15} is His, Leu, or Pro; X_{16} is Asp or Ser; or combinations of such selections; or

(e) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:5), and the following amino acid positions are independently selected as follows: X_1 is Arg; X_2 is Asn, Asp, Gly, or Pro; X_3 is Gly or Met; X_5 is Trp, Tyr, or Val; X_6 is Asp; X_7 is Asp; X_8 is Leu; X_9 is Leu or Thr; X_{10} is Lys or Thr; X_{11} is Arg or Leu; X_{12} is Thr or Trp; X_{13} is Met or Phe; X_{14} is Val; X_{16} is Met; X_{17} is Arg, His, or Tyr; X_{18} is Asn or His; or combinations of such selections; or

(f) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO:6), and the following amino acid positions are independently selected as follows: X_1 is Gly, Tyr, or Val; X_2 is His or Tyr; X_3 is Asp or Tyr; X_4 is Asp or Gln; X_5 is Leu or Ser; X_6 is Leu or Thr; X_7 is Lys or Thr; X_8 is Leu or Lys; X_9 is Met or Ser; X_{10} is Thr or Leu; X_{11} is Pro or Thr; X_{12} is Arg or Pro; or combinations of such selections; or

(g) said polypeptide includes an amino acid sequence of the following formula: X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO:7), and the following amino acid positions are independently selected as follows: X_1 is Glu or Lys; X_2 is His or Pro; X_3 is Tyr; X_4 is Asp or Gln; X_5 is Asn or Thr; X_6 is Asp or Pro; X_7 is Ile or Pro; X_8 is Leu or Thr; X_9 is Lys; X_{10} is Gly or Met; X_{11} is Ala or Thr; X_{12} is Arg or His; X_{13} is His; or combinations of such selections.

13. (Original) The BLyS binding polypeptide according to claim 11, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:20-162 as depicted in Tables 1-8.

14. (Original) The BLyS binding polypeptide according to claim 11, comprising an amino acid sequence selected from the group consisting of:

AGKEPCYFYWECAVSGPGPEGGGK (SEQ ID NO:163),
AGVPFCDLLTKJICFEAGPGPEGGGK (SEQ ID NO:164),
GSSRLCHMDELTHVCVHFAPPGPEGGGK (SEQ ID NO:165),
GDGGNCYTDSLTKLHFCMGDEPGPEGGGK (SEQ ID NO:166),
GYDVLTKLYFVPGGPGPEGGGK (SEQ ID NO:167), and
WTDSLTGLWFPDGGPGPEGGGK, (SEQ ID NO:168).

15 – 23. (canceled)

24. (Original) A method for detecting BLyS or a BLyS-like polypeptide in a solution suspected of containing it comprising:

(a) contacting said solution with a polypeptide according to any of claims 1, 9 or 11, and (b) determining whether binding has occurred between said polypeptide and BLyS or a BLyS-like polypeptide.

25. (Currently amended) A method for purifying BLyS or a BLyS-like polypeptide comprising:

~~(a) immobilizing a binding polypeptide according to any of claims 1, 9 or 11 on a solid support~~;

~~(b)~~ contacting a solution containing BLyS or a BLyS-like polypeptide ~~with said support~~ to a support that comprises, immobilized thereon, a BLyS polypeptide according to claims 1, 9, or 11; and, ~~thereafter,~~

~~(c)~~ separating the solution from said support.

26. (Currently amended) BLyS separation media comprising:

(a) a chromatographic matrix material, and, immobilized thereon,

(b) a BLyS binding molecule comprising a BLyS binding polypeptide as defined in any of claims 1, 9, or 11.

27. (Original) The BLyS separation media according to claim 26, comprising:

(a) a chromatographic matrix material, and, immobilized thereon,

(b) a BLyS binding molecule comprising a BLyS binding polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:20-162 and 186-435, as depicted in Tables 1-8 and 14.

28. (Currently amended) A method for separating BLyS or a BLyS-like polypeptide from a solution containing it comprising:

(a) contacting said solution with separation media as defined in claim 26[[,]];

(b) removing unbound material[[,]]; and

(c) eluting bound BLyS or BLyS-like polypeptide from said separation media.

29. (Original) A polynucleotide encoding a BLyS binding polypeptide comprising the amino

acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.

30. (Original) The polynucleotide according to claim 29, wherein Xaa is Pro or Ser.

31. (Currently amended) The polynucleotide according to claim 29, wherein said polypeptides comprises the amino acid sequence: X_1-X_2-Asp-X_4-Leu-Thr-X_7-Leu-X_9-X_{10} (SEQ ID NO:448),

wherein

X_1 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X_2 is Tyr, Phe, Glu, Cys, **or** Asn;

X_4 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X_7 is Lys, Asn, Gln, Gly, or Arg;

X_9 is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and

X_{10} is Leu, Phe, Val, Ile, or His.

32. (Original) The polynucleotide according to claim 31, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

33. (Currently amended) The polynucleotide according to claim 31, wherein said polypeptide comprises the amino acid sequence: Ala-X_2-X_3-X_4-Asp-X_6-Leu-Thr-X_9-Leu-X_{11}-X_{12}-X_{13}-X_{14} (SEQ ID NO: 447),

wherein

X_2 is any amino acid except Arg;

X_3 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X_4 is Tyr, Phe, Glu, Cys, **or** Asn;

X_6 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X_9 is Lys, Asn, Gln, Gly, or Arg;

X_{11} is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X_{12} is Leu, Phe, Val, Ile, or His;

X_{13} is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X_{14} is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

34. (Original) The polynucleotide according to claim 31, encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:186-435 as depicted in Table 14.

35. (Currently amended) A polynucleotide encoding a BLyS binding polypeptide of the formula:

(A) X_1-X_2-X_3-Cys-X_5-Phe-X_7-Trp-Glu-Cys-X_{11}-X_{12}-X_{13} (SEQ ID NO:1),

wherein

X_1 is Ala, Asn, Lys, or Ser;

X_2 is Ala, Glu, Met, Ser, or Val;

X_3 is Ala, Asn, Lys, or Pro;

X_5 is Phe, Trp, or Tyr;

X_7 is Pro or Tyr;

X_{11} is Ala, Gln, His, Phe, or Val;

X_{12} is Asn, Gln, Gly, His, Ser, or Val; and

X_{13} is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (SEQ ID NO:2),

wherein

X_1 is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X_2 is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X_5 is Asp, Ile, Leu, or Tyr;

X_6 is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X_7 is His, Leu, Lys, or Phe;

X_8 is Leu, Pro, or Thr;

X_9 is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X_{10} is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X_{12} is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X_{13} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X_{14} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (SEQ ID NO:3),

wherein

X_1 is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X_2 is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X_3 is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X_5 is Asn, Asp, Pro, Ser, or Thr;

X_6 is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X_7 is Ala, Ile, Leu, Pro, Thr, or Val;

X_8 is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X_9 is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X_{10} is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X_{11} is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X_{13} is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X_{14} is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X_{15} is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9X_{10}-X_{11}-X_{12}-Cys-X_{14}-X_{15}-X_{16} (SEQ ID NO:4),

wherein

X_1 is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X_2 is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X_3 is Asn, Asp, Leu, Pro, Ser, or Val;

X_5 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X_6 is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X_7 is Asp, His, Leu, or Ser;

X_8 is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X_9 is Ala, Arg, Asn, or Leu;

X_{10} is Ile, Leu, Met, Pro, Ser, or Thr;

X_{11} is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X_{12} is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X_{14} is Asp, Gly, Leu, Phe, Tyr, or Val;

X_{15} is Asn, His, Leu, Pro, or Tyr; and

X_{16} is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:5),

wherein

X_1 is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X_2 is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X_3 is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp, or Val;

X_5 is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X_6 is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X_8 is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;

X_9 is Asp, Leu, Pro, Thr, or Val;

X_{10} is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp, or Tyr;

X_{11} is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;

X_{12} is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;

X_{13} is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;

X_{14} is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;

X_{16} is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;

X_{17} is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp, or Tyr; and

X_{18} is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F) X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12} (SEQ ID NO:6),

wherein

X_1 is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;

X_2 is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;

X_3 is Ala, Asp, Lys, Phe, Thr, Trp, or Tyr;

X_4 is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;

X_5 is Asp, Leu, Lys, Phe, Pro, Ser, or Val;

X_6 is His, Ile, Leu, Pro, Ser, or Thr;

X_7 is Arg, Gly, His, Leu, Lys, Met, or Thr;

X_8 is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;

X_9 is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;

X_{10} is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;

X_{11} is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and

X_{12} is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G) X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13} (SEQ ID NO:7),

wherein

X_1 is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;

X_2 is Arg, Gln, His, Ile, Leu, or Pro;

X_3 is Asp, Gly, Ile, Lys, Thr, Tyr, or Val;

X_4 is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;

X_5 is Asn, Asp, His, Ile, Leu, Met, Pro, Thr, or Val;

X_6 is Asp, Glu, His, Leu, Lys, Pro, or Val;

X_7 is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;

X_8 is Gln, Gly, His, Leu, Met, Ser, or Thr;

X_9 is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;

X_{10} is Ala, Gly, Ile, Leu, Lys, Met, or Phe;

X_{11} is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;

X_{12} is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and

X_{13} is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

36 - 38. (canceled)

39. (New) The polypeptide according to claim 9, wherein the polypeptide comprises an amino acid sequence according to formula H.

40. (New) The polypeptide according to claim 39, wherein the polypeptide comprises X_1-X_2-X_3-Cys-X_5-Phe-X_7-Trp-Glu-Cys-X_{11}-X_{12}-X_{13} (SEQ ID NO:1),
wherein
X_1 is Ala, Asn, Lys, or Ser;
X_2 is Ala, Glu, Met, Ser, or Val;
X_3 is Ala, Asn, Lys, or Pro;
X_{11} is Ala, Gln, His, Phe, or Val;
X_{12} is Asn, Gln, Gly, His, Ser, or Val; and
X_{13} is Ala, Asn, Gly, Ile, Pro, or Ser.

41. (New) The polypeptide according to claim 40, wherein X_3 is Lys.

42. (New) The polypeptide according to claim 39, wherein X_5 is Tyr.

43. (New) The polypeptide according to claim 39, wherein X_7 is Tyr.

44. (New) The polypeptide according to claim 39, wherein X_5 is Tyr; and X_7 is Tyr.

45. (New) The polypeptide according to claim 39, that comprises SEQ ID NO:22, 23, 24, 25, or 26.

46. (New) The polypeptide according to claim 39, that comprises SEQ ID NO:27.

47. (New) The BLyS binding polypeptide according to claim 39, wherein the polypeptide comprises the sequence AGKEPCYFYWECAVSGPGPEGGGK (SEQ ID NO:163).

48. (New) The BLyS binding polypeptide of claim 9, wherein the polypeptide binds BLyS with an affinity less than 3 μM.

49. (New) The BLyS binding polypeptide of claim 39, wherein the polypeptide binds BLyS with an affinity less than 3 μM.

50. (New) The BLyS binding polypeptide of claim 40, wherein the polypeptide binds BLyS with an affinity less than 3μM.

51. (New) The BLyS binding polypeptide of claim 9, wherein the polypeptide binds BLyS at least 12-fold better than the polypeptide binds strepavidin.

52. (New) The BLyS binding polypeptide of claim 39, wherein the polypeptide binds BLyS at least 12-fold better than the polypeptide binds strepavidin.

53. (New) The BLyS binding polypeptide of claim 9, that comprises an amino acid sequence according to formula I.

54. (New) The BLyS binding polypeptide of claim 53, that comprises SEQ ID NO:28.

55. (New) A method for purifying BLyS or a BLyS-like polypeptide, the method comprising:

contacting a solution containing BLyS or a BLyS-like polypeptide to a support that comprises, immobilized thereon, a BlyS binding polypeptide according to claim 46 or 47; and,

separating the solution from the support.

56. (New) A nucleic acid comprising a sequence encoding the polypeptide of claim 9, 46, or 47.